

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 101817248A
Source: IFW16
Date Processed by STIC: 2/10/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 02/10/2006

PATENT APPLICATION: US/10/817,248A

TIME: 08:15:26

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\02102006\J817248A.raw

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4 <110> APPLICANT: Abdel-Meguid, Sherin S.
5     Babine, Robert E.
6     Deng, Hongfeng
7     Jin, Lei
8     Lin, Jian
9     Magee, Scott R.
10    Meyers, Harold V.
11    Pandey, Pramod
12    Rynkiewicz, Michael J.
13    Weaver, David T.
14    Gho, Zihong
15    Bannister, Thomas D.
17 <120> TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT OF
18    THROMBOSIS
20 <130> FILE REFERENCE: 50201/003002
22 <140> CURRENT APPLICATION NUMBER: US 10/817,248A
23 <141> CURRENT FILING DATE: 2004-04-02
25 <150> PRIOR APPLICATION NUMBER: US 60/459,910
26 <151> PRIOR FILING DATE: 2003-04-02
28 <160> NUMBER OF SEQ ID NOS: 15
30 <170> SOFTWARE: FastSEQ for Windows Version 4.0
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 625
34 <212> TYPE: PRT
35 <213> ORGANISM: Homo sapiens
37 <400> SEQUENCE: 1
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41           20           25           30
42 Gly Asp Ile Thr Thr Val Phe Thr Pro Ser Ala Lys Tyr Cys Gln Val
43           35           40           45
44 Val Cys Thr Tyr His Pro Arg Cys Leu Leu Phe Thr Phe Thr Ala Glu
45           50           55           60
46 Ser Pro Ser Glu Asp Pro Thr Arg Trp Phe Thr Cys Val Leu Lys Asp
47 65           70           75           80
48 Ser Val Thr Glu Thr Leu Pro Arg Val Asn Arg Thr Ala Ala Ile Ser
49           85           90           95
50 Gly Tyr Ser Phe Lys Gln Cys Ser His Gln Ile Ser Ala Cys Asn Lys
51           100          105          110
52 Asp Ile Tyr Val Asp Leu Asp Met Lys Gly Ile Asn Tyr Asn Ser Ser
53           115          120          125
54 Val Ala Lys Ser Ala Gln Glu Cys Gln Glu Arg Cys Thr Asp Asp Val

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55      130      135      140
56 His Cys His Phe Phe Thr Tyr Ala Thr Arg Gln Phe Pro Ser Leu Glu
57 145      150      155      160
58 His Arg Asn Ile Cys Leu Leu Lys His Thr Gln Thr Gly Thr Pro Thr
59      165      170      175
60 Arg Ile Thr Lys Leu Asp Lys Val Val Ser Gly Phe Ser Leu Lys Ser
61      180      185      190
62 Cys Ala Leu Ser Asn Leu Ala Cys Ile Arg Asp Ile Phe Pro Asn Thr
63      195      200      205
64 Val Phe Ala Asp Ser Asn Ile Asp Ser Val Met Ala Pro Asp Ala Phe
65      210      215      220
66 Val Cys Gly Arg Ile Cys Thr His His Pro Gly Cys Leu Phe Phe Thr
67 225      230      235      240
68 Phe Phe Ser Gln Glu Trp Pro Lys Glu Ser Gln Arg Asn Leu Cys Leu
69      245      250      255
70 Leu Lys Thr Ser Glu Ser Gly Leu Pro Ser Thr Arg Ile Lys Lys Ser
71      260      265      270
72 Lys Ala Leu Ser Gly Phe Ser Leu Gln Ser Cys Arg His Ser Ile Pro
73      275      280      285
74 Val Phe Cys His Ser Ser Phe Tyr His Asp Thr Asp Phe Leu Gly Glu
75      290      295      300
76 Glu Leu Asp Ile Val Ala Ala Lys Ser His Glu Ala Cys Gln Lys Leu
77 305      310      315      320
78 Cys Thr Asn Ala Val Arg Cys Gln Phe Phe Thr Tyr Thr Pro Ala Gln
79      325      330      335
80 Ala Ser Cys Asn Glu Gly Lys Gly Lys Cys Tyr Leu Lys Leu Ser Ser
81      340      345      350
82 Asn Gly Ser Pro Thr Lys Ile Leu His Gly Arg Gly Gly Ile Ser Gly
83      355      360      365
84 Tyr Thr Leu Arg Leu Cys Lys Met Asp Asn Glu Cys Thr Thr Lys Ile
85      370      375      380
86 Lys Pro Arg Ile Val Gly Gly Thr Ala Ser Val Arg Gly Glu Trp Pro
87 385      390      395      400
88 Trp Gln Val Thr Leu His Thr Thr Ser Pro Thr Gln Arg His Leu Cys
89      405      410      415
90 Gly Gly Ser Ile Ile Gly Asn Gln Trp Ile Leu Thr Ala Ala His Cys
91      420      425      430
92 Phe Tyr Gly Val Glu Ser Pro Lys Ile Leu Arg Val Tyr Ser Gly Ile
93      435      440      445
94 Leu Asn Gln Ser Glu Ile Lys Glu Asp Thr Ser Phe Phe Gly Val Gln
95      450      455      460
96 Glu Ile Ile Ile His Asp Gln Tyr Lys Met Ala Glu Ser Gly Tyr Asp
97 465      470      475      480
98 Ile Ala Leu Leu Lys Leu Glu Thr Thr Val Asn Tyr Thr Asp Ser Gln
99      485      490      495
100 Arg Pro Ile Cys Leu Pro Ser Lys Gly Asp Arg Asn Val Ile Tyr Thr
101      500      505      510
102 Asp Cys Trp Val Thr Gly Trp Gly Tyr Arg Lys Leu Arg Asp Lys Ile
103      515      520      525

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104 Gln Asn Thr Leu Gln Lys Ala Lys Ile Pro Leu Val Thr Asn Glu Glu
105      530      535      540
106 Cys Gln Lys Arg Tyr Arg Gly His Lys Ile Thr His Lys Met Ile Cys
107 545      550      555      560
108 Ala Gly Tyr Arg Glu Gly Gly Lys Asp Ala Cys Lys Gly Asp Ser Gly
109      565      570      575
110 Gly Pro Leu Ser Cys Lys His Asn Glu Val Trp His Leu Val Gly Ile
111      580      585      590
112 Thr Ser Trp Gly Glu Gly Cys Ala Gln Arg Glu Arg Pro Gly Val Tyr
113      595      600      605
114 Thr Asn Val Val Glu Tyr Val Asp Trp Ile Leu Glu Lys Thr Gln Ala
115      610      615      620
116 Val
117 625
120 <210> SEQ ID NO: 2
121 <211> LENGTH: 624
122 <212> TYPE: PRT
123 <213> ORGANISM: Oryctolagus cuniculus
125 <400> SEQUENCE: 2
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127 1      5      10      15
128 Ser Gly Glu Cys Val Ile Lys Leu Phe Ser Asp Ile Tyr Phe Gln Gly
129      20      25      30
130 Gly Asp Ile Thr Thr Val Tyr Thr Pro Asn Ala Lys His Cys Gln Val
131      35      40      45
132 Val Cys Thr Tyr His Pro Arg Cys Leu Leu Phe Thr Phe Met Ala Glu
133      50      55      60
134 Ser Ser Val Asp Ser Thr Lys Trp Phe Ser Cys Ile Leu Lys Asp Ser
135 65      70      75      80
136 Val Thr Glu Ser Leu Pro Lys Val Asn Met Thr Gly Ala Ile Ser Gly
137      85      90      95
138 Tyr Ser Phe Lys Gln Cys Pro His Gln Leu Ser Ala Cys Asn Lys Asp
139      100     105     110
140 Ile Tyr Val Asp Leu Asp Met Gln Gly Met Asn Tyr Asn Gly Ser Val
141      115     120     125
142 Thr Lys Asn Ala Gln Glu Cys Gln Glu Arg Cys Thr Asn Asp Ala His
143      130     135     140
144 Cys His Phe Phe Thr Tyr Ala Thr Arg Gln Phe Pro Ser Ala Glu His
145 145      150     155     160
146 Arg Asn Ile Cys Leu Leu Lys Tyr Thr Gln Thr Gly Ala Pro Thr Gly
147      165     170     175
148 Ile Arg Lys Leu Lys Lys Val Val Ser Gly Phe Ser Leu Lys Ser Cys
149      180     185     190
150 Ala Leu Ser Asn Leu Ala Cys Ile Arg Asp Ile Phe Pro Ser Thr Val
151      195     200     205
152 Phe Ala Asp Asn Asn Ile Asp Ser Val Val Ala Pro Asp Ala Leu Val
153      210     215     220
154 Cys Arg Arg Ile Cys Thr His His Pro Asn Cys Leu Phe Phe Thr Phe
155 225      230     235     240

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156 Phe Ser Gln Glu Trp Pro Lys Glu Ser His Arg Asn Leu Cys Leu Leu
157          245          250          255
158 Lys Thr Ser Glu Ser Gly Leu Pro Ser Thr Arg Ile His Lys Asn Gln
159          260          265          270
160 Ala Leu Ser Gly Phe Ser Leu Gln Asn Cys Arg His Ser Ile Pro Val
161          275          280          285
162 Phe Cys His Ser Ser Phe Tyr Tyr Asp Thr Asp Phe Leu Gly Glu Glu
163          290          295          300
164 Leu Asp Ile Val Asp Val Lys Gly His Glu Ala Cys Gln Lys Met Cys
165 305          310          315          320
166 Thr Ser Ala Ile Arg Cys Gln Phe Phe Thr Tyr Ser Ser Ser Gln Glu
167          325          330          335
168 Ser His Asn Lys Gly Lys Gly Thr Cys Tyr Leu Lys Leu Ser Ser Asn
169          340          345          350
170 Gly Ser Pro Thr Lys Ile Leu His Gly Arg Gly Gly Ile Ser Gly Tyr
171          355          360          365
172 Thr Leu Arg Leu Cys Lys Met Asp Asn Val Cys Thr Thr Lys Ile Lys
173          370          375          380
174 Pro Arg Ile Val Gly Gly Ser Ala Ser Leu Pro Gly Glu Trp Pro Trp
175 385          390          395          400
176 Gln Val Thr Leu His Thr Val Ser Pro Thr Gln Arg His Leu Cys Gly
177          405          410          415
178 Gly Ser Ile Ile Gly Asn Gln Trp Ile Leu Thr Ala Ala His Cys Phe
179          420          425          430
180 Tyr Gly Ile Glu Ser Pro Lys Ile Leu Arg Val Tyr Gly Gly Ile Leu
181          435          440          445
182 Asn Gln Ser Glu Ile Lys Glu Asp Thr Ala Phe Phe Gly Val Gln Glu
183          450          455          460
184 Ile Ile Ile His Asp Gln Tyr Lys Thr Ala Glu Ser Gly Tyr Asp Ile
185 465          470          475          480
186 Ala Leu Leu Lys Leu Glu Thr Thr Met Asn Tyr Thr Asp Ser Gln Arg
187          485          490          495
188 Pro Ile Cys Leu Pro Ser Lys Gly Asp Arg Asn Val Ile Tyr Thr Asp
189          500          505          510
190 Cys Trp Val Thr Gly Trp Gly Tyr Arg Lys Leu Arg Asp Lys Ile Gln
191          515          520          525
192 Asn Thr Leu Gln Lys Ala Lys Ile Pro Leu Leu Ser Asn Glu Glu Cys
193          530          535          540
194 Gln Lys Arg Tyr Gln Arg His Glu Ile Thr Ser Gly Met Ile Cys Ala
195 545          550          555          560
196 Gly Tyr Lys Glu Gly Gly Lys Asp Ala Cys Lys Gly Asp Ser Gly Gly
197          565          570          575
198 Pro Leu Ser Cys Lys His Asn Glu Val Trp His Leu Val Gly Ile Thr
199          580          585          590
200 Ser Trp Gly Glu Gly Cys Ala Gln Arg Glu Arg Pro Gly Ile Tyr Thr
201          595          600          605
202 Asn Val Val Lys Tyr Leu Asp Trp Ile Leu Glu Lys Thr Gln Ala Pro
203          610          615          620
206 <210> SEQ ID NO: 3

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207 <211> LENGTH: 624

208 <212> TYPE: PRT

209 <213> ORGANISM: Mus musculus

211 <400> SEQUENCE: 3

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212 Met Thr Ser Leu His Gln Val Leu Tyr Phe Ile Phe Phe Ala Ser Val
213 1 5 10 15
214 Ser Ser Glu Cys Val Thr Lys Val Phe Lys Asp Ile Ser Phe Gln Gly
215 20 25 30
216 Gly Asp Leu Ser Thr Val Phe Thr Pro Ser Ala Thr Tyr Cys Arg Leu
217 35 40 45
218 Val Cys Thr His His Pro Arg Cys Leu Leu Phe Thr Phe Met Ala Glu
219 50 55 60
220 Ser Ser Ser Asp Asp Pro Thr Lys Trp Phe Ala Cys Ile Leu Lys Asp
221 65 70 75 80
222 Ser Val Thr Glu Ile Leu Pro Met Val Asn Met Thr Gly Ala Ile Ser
223 85 90 95
224 Gly Tyr Ser Phe Lys Gln Cys Pro Gln Gln Leu Ser Thr Cys Ser Lys
225 100 105 110
226 Asp Glu Tyr Val Asn Leu Asp Met Lys Gly Met Asn Tyr Asn Ser Ser
227 115 120 125
228 Val Val Lys Asn Ala Arg Glu Cys Gln Glu Arg Cys Thr Asp Asp Ala
229 130 135 140
230 His Cys Gln Phe Phe Thr Tyr Ala Thr Gly Tyr Phe Pro Ser Val Asp
231 145 150 155 160
232 His Arg Lys Met Cys Leu Leu Lys Tyr Thr Arg Thr Gly Thr Pro Thr
233 165 170 175
234 Thr Ile Thr Lys Leu Asn Gly Val Val Ser Gly Phe Ser Leu Lys Ser
235 180 185 190
236 Cys Gly Leu Ser Asn Leu Ala Cys Ile Arg Asp Ile Phe Pro Asn Thr
237 195 200 205
238 Val Leu Ala Asp Leu Asn Ile Asp Ser Val Val Ala Pro Asp Ala Phe
239 210 215 220
240 Val Cys Arg Arg Ile Cys Thr His His Pro Thr Cys Leu Phe Phe Thr
241 225 230 235 240
242 Phe Phe Ser Gln Ala Trp Pro Lys Glu Ser Gln Arg His Leu Cys Leu
243 245 250 255
244 Leu Lys Thr Ser Glu Ser Gly Leu Pro Ser Thr Arg Ile Thr Lys Ile
245 260 265 270
246 His Ala Leu Ser Gly Phe Ser Leu Gln His Cys Arg His Ser Val Pro
247 275 280 285
248 Val Phe Cys His Pro Ser Phe Tyr Asn Asp Thr Asp Phe Leu Gly Glu
249 290 295 300
250 Glu Leu Asp Ile Val Asp Val Lys Gly Gln Glu Thr Cys Gln Lys Thr
251 305 310 315 320
252 Cys Thr Asn Asn Ala Arg Cys Gln Phe Phe Thr Tyr Tyr Pro Ser His
253 325 330 335
254 Arg Leu Cys Asn Glu Arg Asn Arg Arg Gly Arg Cys Tyr Leu Lys Leu
255 340 345 350
256 Ser Ser Asn Gly Ser Pro Thr Arg Ile Leu His Gly Arg Gly Gly Leu

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VERIFICATION SUMMARY

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